ACA Abstract
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Structural evolution and substrate specificity of Family GH31 α-glucosidases and their contribution to starch digestion.

Starch digestion is one of the fundamentally important nutritional processes of the human body that contributes significantly to our total dietary caloric intake. This process is dependant on gastrointestinal enzymatic mechanisms of amylases and alpha-glucosidases. Alpha-glucosidases consist of the small intestinal enzymes maltase glucoamylase (MGAM) and sucrase isomaltase (SI). Through their hydrolytic mechanisms free glucose is liberated from ingested starch. MGAM and SI are members of the Family 31 glycoside hydrolases. Though this family has a varied sequence similarity (15-60% sequence homology) it demonstrates strong structural conservation. A number of family 31 α-glucosidase structures have been solved, providing important structural information that can be related to function. Despite this family of enzymes having a commonly observed mechanism of hydrolyzing starch glycans, it has been reported that these enzymes demonstrate distinct functions. These distinct functions can range from having the ability to hydrolyze α, 1-4 and/or α, 1-6 linkages between glucose residues or hydrolyzing short and/or long linear maltooligosaccharides. By exploring the evolutionary structural changes that have arisen within this family we can observe differences that relate to substrate preference. Our phylogenetic structural analysis reveals key amino acids we believe have contributed to structural differences allowing for the variability in substrate preference observed within Family 31.